Figure 1
Nucleotide Sequence and predicted protein for HLTDG74

```
              10                30                50
-88  GTTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTTCCGGGCTCTGGAGGAGGGT-29


              70                90                110
-28  CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCGTCGCTCCACGTCT   31
 -8                                    M  A  W  L  G  A  S  L  H  V  W   11


              130               150               170
 32  GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA   91
 12   G  W  L  M  L  G  S  C  L  L  A  R  A  Q  L  D  S  D  G  T   31


              190               210               230
 92  CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCGAAAGTACAATGTGAACTCA  151
 32   I  T  I  E  E  Q  I  V  L  V  L  K  A  K  V  Q  C  E  L  N   51


              250               270               290
152  ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTTCCCTGAATGGGATGGACTCA  211
 52   I  T  A  Q  L  Q  E  G  E  G  N  C  F  P  E  W  D  G  L  I   71


              310               330               350
212  TTTGTTGGCCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATTT  271
 72   C  W  P  R  G  T  V  G  K  I  S  A  V  P  C  P  P  Y  I  Y   91


              370               390               410
272  ATGACTTCAACCATAAAGGAGTTGCTTTCCGACACTGTAACCCCAATGGAACATGGGATT  331
 92   D  F  N  H  K  G  V  A  F  R  H  C  N  P  N  G  T  W  D  F  111


              430               450               470
332  TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTTCTGCAGC  391
112   M  H  S  L  N  K  T  W  A  N  Y  S  D  C  L  R  F  L  Q  P  131


              490               510               530
392  CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG  451
132   D  I  S  I  G  K  Q  E  F  C  E  R  L  Y  V  M  Y  T  V  G  151


              550               570               590
452  GCTACTCCATCTCTTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTGGTTACTTCAGAC  511
152   Y  S  I  S  F  G  S  L  A  V  A  I  L  I  I  G  Y  F  R  R  171


              610               630               650
512  GATTGCATTGCACTAGGAACTATATCCACATGCACTTATTTGTGTCTTTCATGCTGAGAG  571
172   L  H  C  T  R  N  Y  I  H  M  H  L  F  V  S  F  M  L  R  A  191


              670               690               710
572  CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG  631
192   T  S  I  F  V  K  D  R  V  V  H  A  H  I  G  V  K  E  L  E  211
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325800-458

FIGURE 1   1/3   10 6

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              730               750                770
632  AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT  691
212    S  L  I  M  Q  D  D  P  Q  N  S  I  E  A  T  S  V  D  K  S  231

              790               810                830
692  CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTTACTTCCTGGCTACAAATT  751
232    Q  Y  I  G  C  K  I  A  V  V  M  F  I  Y  F  L  A  T  N  Y  251

              850               870                890
752  ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTTT  811
252    Y  W  I  L  V  E  G  L  Y  L  H  N  L  I  F  V  A  F  F  S  271

              910               930                950
812  CGGACACCAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG  871
272    D  T  K  Y  L  W  G  F  I  L  I  G  W  G  F  P  A  A  F  V  291

              970               990               1010
872  TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACTTAGTG  931
292    A  A  W  A  V  A  R  A  T  L  A  D  A  R  C  W  E  L  S  A  311

             1030              1050               1070
932  CTGGAGACATCAAGTGGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA  991
312    G  D  I  K  W  I  Y  Q  A  P  I  L  A  A  I  G  L  N  F  I  331

             1090              1110               1130
992  TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG 1051
332    L  F  L  N  T  V  R  V  L  A  T  K  I  W  E  T  N  A  V  G  351

             1150              1170               1190
1052 GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCCTGGTCCTAG 1111
352    H  D  T  R  K  Q  Y  R  K  L  A  K  S  T  L  V  L  V  L  V  371

             1210              1230               1250
1112 TCTTTGGAGTGCATTACATCGTGTTCGTGTGCCTGCCTCACTCCTTCACTGGGCTCGGGT 1171
372    F  G  V  H  Y  I  V  F  V  C  L  P  H  S  F  T  G  L  G  W  391

             1270              1290               1310
1172 GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGTCTA 1231
392    E  I  R  M  H  C  E  L  F  F  N  S  F  Q  G  F  F  V  S  I  411

             1330              1350               1370
1232 TCATCTACTGCTACTGCAATGGAGAGGTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT 1291
412    I  Y  C  Y  C  N  G  E  V  Q  A  E  V  K  K  M  W  S  R  W  431

             1390              1410               1430
1292 GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAG 1351
432    N  L  S  V  D  W  K  R  T  P  P  C  G  S  R  R  C  G  S  V  451

             1450              1470               1490
1352 TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT 1411
452    L  T  T  V  T  H  S  T  S  S  Q  S  Q  V  A  A  A  H  A  W  471

             1510              1530               1550
```
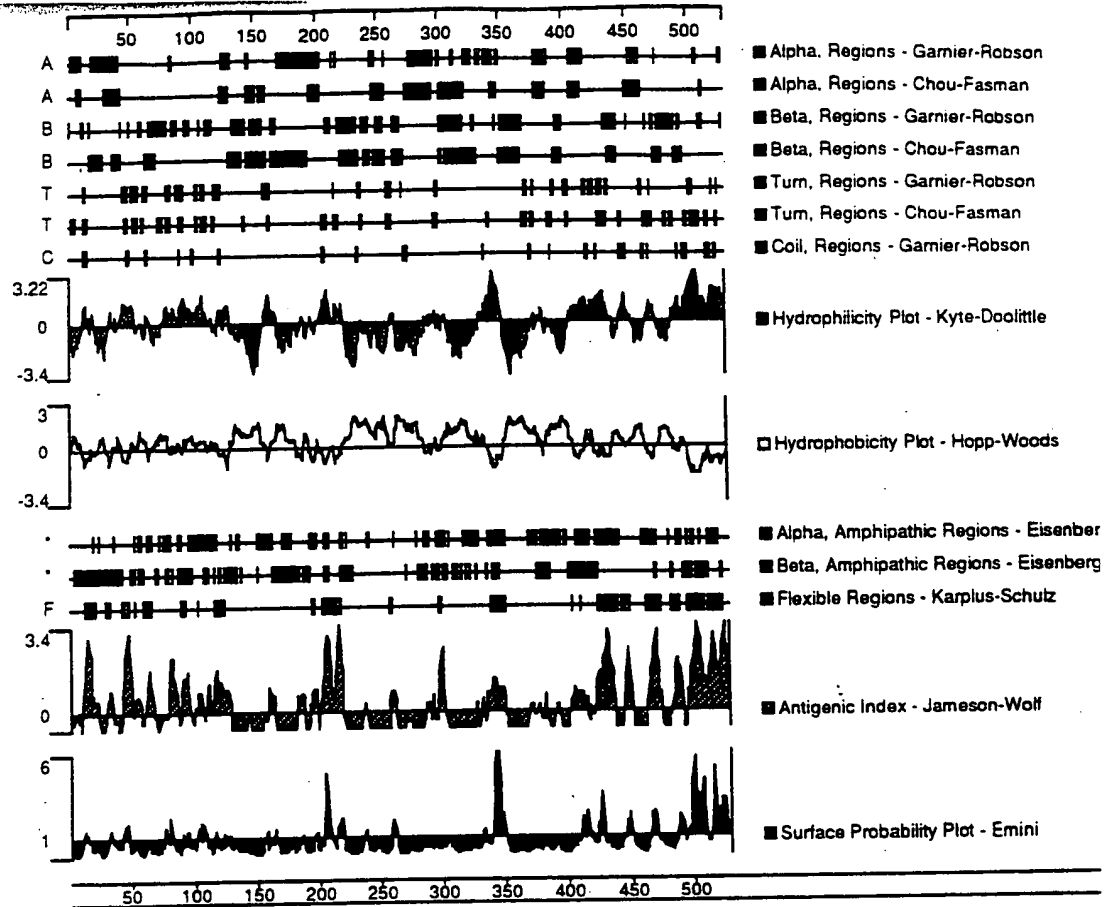
325800-458

~~Page 10~~

2 of 2

FIGURE 1 2/3

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       1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC 1471
        472   C  L  S  L  A  K  L  P  R  S  P  A  D  S  L  T  A  T  S  L   491

                 1570            1590              1610
       1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA 1531
        492   Y  L  A  M  S  G  V  T  Q  S  R  T  A  S  H  T  L  S  T  R   511

                 1630            1650              1670
       1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA 1591
        512   S  N  K  E  D  S  G  R  Q  R  D  D  I  L  M  E  K  P  S  R   531

                 1690            1710              1730
       1592 GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAAACTGAGGATGTTCTCT 1651
        532   P  M  E  S  N  P  D  T  E  G                                541

                 1750            1770              1790
       1652 GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC 1711

                 1810            1830              1850
       1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA 1771

                 1870            1890              1910
       1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG 1831

                 1930            1950              1970
       1832 TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT 1891

                 1990
       1892 GGTATTTGCTCTGTGATTGTTCA                                       1914
```

FIGURE 2   1/1

325800-458

```
                                                      Readi    High  Probability
                       Segment Pairs:             F.. .. Score  P(N.          N

gp|M74445|OPOPTHR_1   parathyroid hormone receptor [Di...  +3   59~  S.2e-204   6
pir|S|A39286          parathyroid hormone / parathyroi...  +3   59~  2.9e-203   6
gp|L04308|HUMPTHR_1   parathyroid hormone receptor [Ho...  +3   580  6.7e-190   5
pir|S|S29610          parathyroid hormone receptor - h...  +3   580  6.1e-189   5
gp|M77184|RATPATHYR_1 parathyroid hormone receptor [Ra...  +3   5~6  ~.7e-188   5
gp|X78936|MMPHRPR_1   parathyroid hormone/parathyroid ...  +3   576  7.7e-188   5
pir|S|A42698          parathyroid hormone and parathyr...  +3   576  7.7e-188   5
gp|L34611|MUSPTHR06_1 parathyroid hormone/parathyroid ...  +3   576  4.1e-174   5
gp|U11087|HSV1RG9_1   vasoactive intestinal peptide 1 ...  +3   319  1.2e-98    5
gp|M86835|RATVASREC_1 vasoactive intestinal polypeptid...  +3   254  3.1e-91    5
```

WARNING: Descriptions of 49 database sequences were not reported due to the
limiting value of parameter V = 10.

>gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana]
            Length = 585

  Plus Strand HSPs:

 Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT 908
               I +++ +   E   DK+ ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+
Sbjct: 253 ITEEELRAFTEPPPADKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF 1088
               KYLWGF L GWG PA FVA W   RATLA+   CW+LS+G+ KWI Q PILAAI +NFILF
Sbjct: 313 KYLWGFTLFGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVLVFGVHYIVFVCLPHS 1244
               +N +RVLATK+ ETNA   DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
Sbjct: 373 INIIRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHYIVFMATPYT 424

 Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW 446
               +G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ +   N+TW
Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHKGRAYRRCDSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476
               ANYS+C++FL
Sbjct: 162 ANYSECVKFL 171

 Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677
               ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
Sbjct: 177 EREVFDRLGMIYTVGYSISLGSLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESLIMQD 740
               KD V+++ + E+E + ++
Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

 Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS 1424
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5 of 6

FIGURE 3   1/2   325800-458

```
GFFV+IIYC+CNGEVQAE+KK W     L++D+KR    GS
GFFVAIIYCFCNGEVQAEIKKSW     LALDFKRKARSGS 425
```

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

```
Query:   159 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269
             A +D+D  IT EEQI+L+  A+ QCE +   L+ E
Sbjct:    24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60
```

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

```
Query:  1508 ISGKAAKIASRQPDSHITLPGYV 1576
             +S + A A    + H  LPGYV
Sbjct:   512 LSPRLAPGAGASANGHHQLPGYV 534
```

FIGURE   3   2/2 325800-458